<110> Richter, Mark M
        Powell, Michael J
        Belisle, Christopher M

<120> Assays Employing Electrochemiluminescent Labels and
        Electrochemiluminescence Quenchers

<130> 337462000600

<140> 09/074,472
<141> 1998-05-07

<160> 16

<170> PatentIn Ver. 2.0

<210> 1
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 1
atcgtgcggt ggttgaactg                                                    20

<210> 2
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> modified_base
<222> (1)
<223> Ru(bpy),(subscript 3, superscript
        +2)-containing group is bound to the adenine

<220>
<221> modified_base
<222> (20)
<223> Biotin-containing group is bound to guanine

<400> 2
atcgtgcggt ggttgaactg                                                    20

<210> 3
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> modified_base
<222> (1)
<223> Ru(bpy)[subscript 3, superscript
    +2]-containing group is bound to cytosine

<220>
<221> modified_base
<222> (21)
<223> Biotin-containing group is bound to thymine

<220>
<221> modified_base
<222> (4)
<223> n denotes "amine modified C(subscript 6)-dT" - modified thymine residue


<400> 3
cagntccaac caaccgcacg t                                        21

<210> 4
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> modified_base
<222> (1)
<223> Ru(bpy)[subscript 3, superscript
    +2]-containing group is bound to cytosine

<220>
<221> modified_base
<222> (21)
<223> n denotes "amine modified C(subscript 6)-dT" - modified thymine residue

<220>
<221> modified_base
<222> (21)
<223> Biotin-containing group is bound to the modified thymine residue at
position 21

<400> 4
cagttccaac caaccgcacg n                                        21

<210> 5
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

2

<223> Synthetic construct

<220>
<221> modified_base
<222> (1)
<223> Ru(bpy)[subscript 3, superscript
+2]-containing group is bound to cytosine

<220>
<221> modified_base
<222> 21
<223> Thymine has 5 "L" groups bound to it (L="Label On" - a commercially available reagent)

<220>
<221> modified_base
<222> (21)
<223> Biotin-containing group is attached to the last "L" group bound to Thymine


<400> 5
cagttccaac caaccgcacg t                                              21


<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> modified_base
<222> (1)
<223> Ru(bpy)[subscript 3, superscript
+2]-containing group is bound to cytosine

<220>
<221> modified_base
<222> (4)
<223> n denotes "amine modified C(subscript 6)-dT"-modified thymine residue; modified thymine has a benzoquinone moiety attached


<220>
<221> modified_base
<222> (22)
<223> Biotin-containing group is bound to thymine


<400> 6
cagntccaac caaccgcacg t                                              21

<210> 7
<211> 21
<212> DNA

3

<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> modified_base
<222> (1)
<223> Ru(bpy)[subscript 3, superscript
     +2]-containing group is bound to cytosine

<220>
<221> modified_base
<222> (21)
<223> n denotes "amine modified C(subscript 6)-dT"-modified thymine residue;
modified thymine has benzoquinone moiety attached


<220>
<221> modified_base
<222> (21)
<223> Biotin-containing group is bound to the modified thymine


<400> 7
cagttccaac caaccgcacg n                                              21

<210> 8
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> modified_base
<222> (1)
<223> Ru(bpy)[subscript 3, superscript
     +2]-containing group is bound to cytosine

<220>
<221> modified_base
<222> 21
<223> Thymine has 5 "L" groups bound to it (L="Label On" - a commercially
available reagent; each "L" group has a benzoquinone moiety attached; last
benzoquinone moiety has biotin-containing group attached


<400> 8
cagttccaac caaccgcacg t                                              21

<210> 9
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> modified_base
<222> (1)
<223> "5'-amino modifier" is bound to adenine

<220>
<221> modified_base
<222> (23)
<223> n denotes "carboxyl modified dT"-modified thymine residue
<220>
<221> modified_base
<222> (23)
<223> Biotin-containing group is bound to the modified thymine

<400> 9
acgccactgg atccacagtt agn                                    23

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> modified_base
<222> (24)
<223> n denotes "carboxyl modified dT"-modified thymine residue

<220>
<221> modified_base
<222> (24)
<223> Biotin-containing group is bound to the modified thymine

<220>
<221> modified_base
<222> (19)
<223> n is unknown.

<400> 10
aacgccactg gatccacant tagn                                   24

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> modified_base
<222> (1)

<223> n denotes "amine modified C(subscript 6)-dT"- modified thymine residue

<220>
<221> modified_base
<222> (26)
<223> n denotes "carboxyl modified dT"-modified thymine residue


<220>
<221> modified_base
<222> (26)
<223> Biotin-containing group is bound to the modified thymine
<220>

<400> 11
nttgcggtga cctaggtgtc aatcan                                    26

<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> modified_base
<222> (25)
<223> n denotes "carboxyl modified dT"-modified thymine residue


<220>
<221> modified_base
<222> (25)
<223> Biotin-containing group is bound to the modified thymine
<220> .

<400> 12
ttgcggtgac ctaggtgtcc atcan                                     25

<210> 13
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> modified_base
<222> (1)
<223> Adedine has bound to it a "5'-amino modifier" and a  "quenching moiety"

<220>
<221> modified_base
<222> (23)
<223> n denotes "carboxyl modified dT"-modified thymine residue

```
<220>
<221> modified_base
<222> (23)
<223> Ru(bpy) [subscript 3, superscript
     +2]-containing group and biotin containing group is bound to the modified
     thymine

<400> 13
acgccactgg atccacagtt agn                                        23

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> modified_base
<222> (24)
<223> n denotes "carboxyl modified dT"-modified thymine residue


<220>
<221> modified_base
<222> (24)
<223> Ru(bpy) [subscript 3, superscript
     +2]-containing group and biotin containing group is bound to the modified
thymine

<220>
<221> modified_base
<222> (19)
<223> n is unknown.

<400> 14
aacgccactg gatccacant tagn                                       24

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> modified_base
<222> (1)
<223> n denotes "amine modified C, (subscript 6)-dT"-modified thymine with
quenching moiety attached

<220>
<221> modified_base
```

<222> (26)
<223> n denotes "carboxyl modified dT"-modified thymine residue


<220>
<221> modified_base
<222> (26)
<223> Ru(bpy)[subscript 3, superscript
       +2]-containing group and biotin-containing group is bound to the modified
thymine

<400> 15
nttgcggtga cctaggtgtc aatcan                                        26

<210> 16
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> modified_base
<222> (25)
<223> n denotes "carboxyl modified dT"-modified thymine residue


<220>
<221> modified_base
<222> (25)
<223> Ru(bpy)[subscript 3, superscript +2]-containing group and biotin
containing group is bound to the modified thymine

<400> 16
ttgcggtgac ctaggtgtcc atcan                                         25

# Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: _09/074,472_ |

NOV 15 1999

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS WHICH WERE INSERTED BY PTO SOFTWARE**

1 _____ **Wrapped Nucleics**
The number/text at the end of each line wrapped down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ **Wrapped Aminos**
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ **Incorrect Line Length**
The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.

4 _____ **Misaligned Amino Acid . Numbering**
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.

5 _____ **Non-ASCII**
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ **Variable Length**
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.

7 _____ **Wrong Designation**
Sequence(s) _____ contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)

8 _____ **Skipped Sequences (OLD RULES)**
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ **Skipped Sequences (NEW RULES)**
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ **Use of N's or Xaa's (NEW RULES)**
Use of N's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

11 _____ **Use of <213>Organism (NEW RULES)**
Sequence(s) _____ are missing this mandatory field or its response.
*1-11( possibly more after seg 11)*

12 _____ **Use of <220>Feature (NEW RULES)**
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)

13 _____ **Wrong Format**
File submitted was in the alphabetical heading format of the Old Sequence Rules. This is invalid since the
"Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures"
Federal Register Notice, Vol. 63, No. 104, June 1, 1998, p. 29620
applies to applications filed on or after July 1, 1998.

AKS-Biotechnology Systems Branch- 7/10/98